



SEQUENCE LISTING

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TANAKA, YOSHIKAZU
FUJIWARA, HIROYUKI
NAKAO, MASAHIRO
FUKUI, YUKO
SAKAKIBARA, KEIKO
MIZUTANI, MASAKO
KUSUMI, TAKAAKI

<120> A GENE ENCODING A PROTEIN HAVING ACYL GROUP TRANSFER
ACTIVITY

<130> 47237-0308/US

<140> 08/894,356
<141> 1997-08-18

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<151> 1995-02-17

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Asp Asn Glu Asp Ala Phe Phe Leu Ile Pro Val Asp Leu Arg Pro Arg	
290 295 300	
tta gat ccg ccg gtt cct gaa aat tac ttc ggg aac tgc tta tcg tac	959
Leu Asp Pro Pro Val Pro Glu Asn Tyr Phe Gly Asn Cys Leu Ser Tyr	
305 310 315	
gcg ctg ccg aga atg cgg cgg cga gag ctg gtg gga gag aaa ggg gtg	1007
Ala Leu Pro Arg Met Arg Arg Arg Glu Leu Val Gly Glu Lys Gly Val	
320 325 330 335	
ttt ctg gca gct gag gta atc gcg gcg gag ata aaa aaa agg atc aac	1055
Phe Leu Ala Ala Glu Val Ile Ala Ala Glu Ile Lys Lys Arg Ile Asn	
340 345 350	
gac aag aga ata tta gaa acg gtg gag aaa tgg tcg ccg gag att cgt	1103
Asp Lys Arg Ile Leu Glu Thr Val Glu Lys Trp Ser Pro Glu Ile Arg	
355 360 365	
aaa gcg ttg cag aaa tca tat ttt tcg gtg gca gga tcg agc aag cta	1151
Lys Ala Leu Gln Lys Ser Tyr Phe Ser Val Ala Gly Ser Ser Lys Leu	
370 375 380	
gat ctt tac ggt gca gat ttt gga tgg ggg aag gcg aga aag caa gaa	1199
Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala Arg Lys Gln Glu	
385 390 395	
ata ttg tcg att gat ggg gag aaa tat gca atg acg ctt tgt aaa gcc	1247
Ile Leu Ser Ile Asp Gly Glu Lys Tyr Ala Met Thr Leu Cys Lys Ala	
400 405 410 415	

agg gat ttc gaa gga gga ttg gag gtt tgc ttg tct ttg cct aag gac 1295
 Arg Asp Phe Glu Gly Gly Leu Glu Val Cys Leu Ser Leu Pro Lys Asp
 420 425 430

aaa atg gat gct ttt gct gct tat ttt tca ctg gga att aat ggt 1340
 Lys Met Asp Ala Phe Ala Ala Tyr Phe Ser Leu Gly Ile Asn Gly
 435 440 445

taataaatgt atgtaattaa actaatatta ttatgtaaca attaattaag tgttgagtaa 1400

cgtgaagaat aatccctatt atatatttat gatttgggttc aaataaagtg taaagcctct 1460

tgaaaaaaaa aaaaaaaaaa 1479

<210> 5

<211> 1508

<212> DNA

<213> Senecio cruentus

<220>

<221> CDS

<222> (3)..(1364)

<400> 5

tg aac att ctc gaa cat gcc cga ata tcg gcc ccc tcg ggc acc atc 47
 Asn Ile Leu Glu His Ala Arg Ile Ser Ala Pro Ser Gly Thr Ile
 1 5 10 15

ggc cat cgc tcg tta tct ctt act ttc ttc gac att act tgg cta ctc 95
 Gly His Arg Ser Leu Ser Leu Thr Phe Phe Asp Ile Thr Trp Leu Leu
 20 25 30

ttc cct ccg gtc cac cat ctt ttc ttc tat gac ttt oca cat tct aaa 143
 Phe Pro Pro Val His His Leu Phe Phe Tyr Asp Phe Pro His Ser Lys
 35 40 45

tcc cat ttc atg gac act att gtt ccc agg cta aaa caa tct tta tcg 191
 Ser His Phe Met Asp Thr Ile Val Pro Arg Leu Lys Gln Ser Leu Ser
 50 55 60

gtc act ctt caa cat ttt ttc ccg ttt gct agt aat ttg att gta ttt 239
 Val Thr Leu Gln His Phe Phe Pro Phe Ala Ser Asn Leu Ile Val Phe
 65 70 75

cct aac act gat ggt tcg ggt ttt aat aaa aaa cca gaa ata aaa cac 287
 Pro Asn Thr Asp Gly Ser Gly Phe Asn Lys Lys Pro Glu Ile Lys His
 80 85 90 95

gtt gaa ggt gat tct gtt gtg gtt act ttt gca gaa tgt tgt ctt gac 335
 Val Glu Gly Asp Ser Val Val Val Thr Phe Ala Glu Cys Cys Leu Asp
 100 105 110

ttt aat aat ttg aca gga aat cat cct cga aaa tgt gaa aac ttt tat 383
 Phe Asn Asn Leu Thr Gly Asn His Pro Arg Lys Cys Glu Asn Phe Tyr
 115 120 125

cca	ctt	gta	cct	tca	ttg	gga	aat	gca	atc	aaa	tta	tgt	gat	tgc	gtc	431
Pro	Leu	Val	Pro	Ser	Leu	Gly	Asn	Ala	Ile	Lys	Leu	Cys	Asp	Cys	Val	
		130					135					140				
acg	gtc	cca	ctt	ttt	tca	ctt	caa	gtg	acg	ttt	ttt	ccg	ggc	tgc	ggc	479
Thr	Val	Pro	Leu	Phe	Ser	Leu	Gln	Val	Thr	Phe	Phe	Pro	Gly	Ser	Gly	
	145					150					155					
ata	tca	cta	gga	atg	acg	aat	cat	cat	agc	ctt	ggc	gac	gct	agc	acg	527
Ile	Ser	Leu	Gly	Met	Thr	Asn	His	His	Ser	Leu	Gly	Asp	Ala	Ser	Thr	
160					165					170					175	
cgg	ttc	aac	ttt	ttg	aaa	ggg	tgg	act	tgc	att	att	caa	tct	ggc	gta	575
Arg	Phe	Asn	Phe	Leu	Lys	Gly	Trp	Thr	Ser	Ile	Ile	Gln	Ser	Gly	Val	
				180					185					190		
gat	cgg	tct	ttt	tta	acg	aaa	gga	tct	cca	ccg	gtt	ttt	gat	aga	ttg	623
Asp	Arg	Ser	Phe	Leu	Thr	Lys	Gly	Ser	Pro	Pro	Val	Phe	Asp	Arg	Leu	
			195					200					205			
att	aac	atc	cca	cat	tta	gat	gaa	aat	aag	ttg	aga	cat	aca	agg	ctc	671
Ile	Asn	Ile	Pro	His	Leu	Asp	Glu	Asn	Lys	Leu	Arg	His	Thr	Arg	Leu	
		210					215					220				
gaa	agt	ttt	tat	aaa	cct	tgc	agc	ctt	gtt	ggc	ccc	act	gat	aaa	gtt	719
Glu	Ser	Phe	Tyr	Lys	Pro	Ser	Ser	Leu	Val	Gly	Pro	Thr	Asp	Lys	Val	
	225					230				235						
cgg	tca	acg	ttt	gtg	ttg	acc	cga	act	aat	atc	aat	cta	cta	aag	aaa	767
Arg	Ser	Thr	Phe	Val	Leu	Thr	Arg	Thr	Asn	Ile	Asn	Leu	Leu	Lys	Lys	
240				245						250					255	
aag	gtc	tta	acc	caa	gtg	cca	aac	ttg	gag	tac	atg	tca	tct	ttt	acg	815
Lys	Val	Leu	Thr	Gln	Val	Pro	Asn	Leu	Glu	Tyr	Met	Ser	Ser	Phe	Thr	
				260					265					270		
gta	act	tgt	ggc	tat	ata	tgg	agt	tgc	ata	gcg	aaa	tca	ctc	gta	aaa	863
Val	Thr	Cys	Gly	Tyr	Ile	Trp	Ser	Cys	Ile	Ala	Lys	Ser	Leu	Val	Lys	
			275					280					285			
ata	gga	gaa	aga	aag	ggc	gaa	gac	gag	tta	gaa	cag	ttc	ata	atc	acc	911
Ile	Gly	Glu	Arg	Lys	Gly	Glu	Asp	Glu	Leu	Glu	Gln	Phe	Ile	Ile	Thr	
		290				295						300				
att	gat	tgt	cga	tct	cgt	ctt	gat	cca	cca	att	ccc	aca	gcc	tac	ttt	959
Ile	Asp	Cys	Arg	Ser	Arg	Leu	Asp	Pro	Pro	Ile	Pro	Thr	Ala	Tyr	Phe	
	305					310					315					
ggc	aac	tgt	ggc	gca	cca	tgt	gtc	ccg	acc	tta	aaa	aat	gtc	gtt	ttg	1007
Gly	Asn	Cys	Gly	Ala	Pro	Cys	Val	Pro	Thr	Leu	Lys	Asn	Val	Val	Leu	
320					325					330					335	
act	acg	gaa	aat	ggg	tat	gca	ctt	ggc	gct	aaa	gta	att	gga	gag	tct	1055
Thr	Thr	Glu	Asn	Gly	Tyr	Ala	Leu	Gly	Ala	Lys	Val	Ile	Gly	Glu	Ser	
				340					345					350		

ata tgc aaa atg ata tat aat aag gac gga atc ttg aaa gat gcc gcg 1103
 Ile Cys Lys Met Ile Tyr Asn Lys Asp Gly Ile Leu Lys Asp Ala Ala
 355 360 365
 aga tgg cat gaa cct ttc atg atc ccg gct agg aag att ggt gtt gct 1151
 Arg Trp His Glu Pro Phe Met Ile Pro Ala Arg Lys Ile Gly Val Ala
 370 375 380
 ggt aca cct aag ctc aac ttg tac gac ttt gat ttt ggg tgg ggg aag 1199
 Gly Thr Pro Lys Leu Asn Leu Tyr Asp Phe Asp Phe Gly Trp Gly Lys
 385 390 395
 cgc ata aag tat gag act gtt tca ata gac tat aat acg tcg att tct 1247
 Arg Ile Lys Tyr Glu Thr Val Ser Ile Asp Tyr Asn Thr Ser Ile Ser
 400 405 410 415
 ata aat gca agc aaa aca tca gca caa gat ctt gaa att gga ttg agt 1295
 Ile Asn Ala Ser Lys Thr Ser Ala Gln Asp Leu Glu Ile Gly Leu Ser
 420 425 430
 cta ccg agt atg caa atg gag gcg ttt tct agc atc ttt gat gaa gga 1343
 Leu Pro Ser Met Gln Met Glu Ala Phe Ser Ser Ile Phe Asp Glu Gly
 435 440 445
 tta gag agt caa gtt tca ttg tagatcatcg tccccttttt gtgtgcatca 1394
 Leu Glu Ser Gln Val Ser Leu
 450
 agtttctgtc gtttttatga gttgccactg ttctattctt taagtatacc ttctgactat 1454
 gttttgaaga tgcaacgata taaaatgaaa aaaaaaaaaa aaaaaaaaaa aaaa 1508

<210> 6
 <211> 1521
 <212> DNA
 <213> Lavandula angustifolia

<220>
 <221> CDS
 <222> (3)..(1352)

<400> 6
 tg acc acc ctc ctc gaa tcc tcc cga gtg gcg ccg cct cca ggc acg 47
 Thr Thr Leu Leu Glu Ser Ser Arg Val Ala Pro Pro Pro Gly Thr
 1 5 10 15
 gtg gct gag cag tca ctc ccg ctc acc ttc ttc gac atg acg tgg ctg 95
 Val Ala Glu Gln Ser Leu Pro Leu Thr Phe Phe Asp Met Thr Trp Leu
 20 25 30
 cat ttc cac ccc atg ctt cag ctt ctc ttc tac gaa ctc ccc tgt tcc 143
 His Phe His Pro Met Leu Gln Leu Leu Phe Tyr Glu Leu Pro Cys Ser
 35 40 45

aaa ccc gcc ttc ctc gaa acc gtc gtt ccg aaa ctc aaa caa tcc tta	191
Lys Pro Ala Phe Leu Glu Thr Val Val Pro Lys Leu Lys Gln Ser Leu	
50 55 60	
tct cta acc ctc aaa cac ttc ttc ccc ctt tca tgc aat cta atc tac	239
Ser Leu Thr Leu Lys His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr	
65 70 75	
cct cta tcg ccg gag aaa atg ccg gag ttc cgg tat cag aac ggt gac	287
Pro Leu Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Gln Asn Gly Asp	
80 85 90 95	
tcg gtt tct ttc acg att atg gag tct gtc gga gat cat ccg cat tcc	335
Ser Val Ser Phe Thr Ile Met Glu Ser Val Gly Asp His Pro His Ser	
100 105 110	
gct cat aaa tac tac tgc ttt gcc cct agc gac gat tat gaa gat ctc	383
Ala His Lys Tyr Cys Phe Ala Pro Ser Asp Asp Tyr Glu Asp Leu	
115 120 125	
cag ctg ccg ccg ata gtc gag gaa tct gat cgg aaa ttg ttt caa gtt	431
Gln Leu Pro Pro Ile Val Glu Glu Ser Asp Arg Lys Leu Phe Gln Val	
130 135 140	
tta gcc gtg caa gtg act ctg ttt ccc ggt cgc ggg gtg tgc atc gga	479
Leu Ala Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Cys Ile Gly	
145 150 155	
ata acg acg cac cac acc gtt agc gat gct cca tcg ttt gta ggg ttt	527
Ile Thr Thr His His Thr Val Ser Asp Ala Pro Ser Phe Val Gly Phe	
160 165 170 175	
atg aag agt tgg gct tcc atc act aaa ttc gga gga gat gat gaa ttc	575
Met Lys Ser Trp Ala Ser Ile Thr Lys Phe Gly Gly Asp Asp Glu Phe	
180 185 190	
ttg gac gga aaa ggt gaa tgt ttg ccg gtt ttc gac cga tcg ctc gtg	623
Leu Asp Gly Lys Gly Glu Cys Leu Pro Val Phe Asp Arg Ser Leu Val	
195 200 205	
aat tat ccg cct aaa ttg gac aca tat tta tgg aac aac gcg cag aaa	671
Asn Tyr Pro Pro Lys Leu Asp Thr Tyr Leu Trp Asn Asn Ala Gln Lys	
210 215 220	
cgt ccg ttg gaa tcg cag cat cca tct tta ccg acg gat cgg att cga	719
Arg Pro Leu Glu Ser Gln His Pro Ser Leu Pro Thr Asp Arg Ile Arg	
225 230 235	
gct acc tac ctt ttc acc caa tct gaa att aag aaa ttg aag ggt ttg	767
Ala Thr Tyr Leu Phe Thr Gln Ser Glu Ile Lys Lys Leu Lys Gly Leu	
240 245 250 255	
att cag aga aaa gcc cca aat gta gtt aat ctc tct tcc ttc gtc gcg	815
Ile Gln Arg Lys Ala Pro Asn Val Val Asn Leu Ser Ser Phe Val Ala	
260 265 270	

atc gca gct tat atc tgg acc ggc atc gcc aaa tcg gtc gga gat tac	863
Ile Ala Ala Tyr Ile Trp Thr Gly Ile Ala Lys Ser Val Gly Asp Tyr	
275 280 285	
aaa gac gtg gat gac gac aaa cgc gct ttc ttt tta att ccg atc gat	911
Lys Asp Val Asp Asp Asp Lys Arg Ala Phe Phe Leu Ile Pro Ile Asp	
290 295 300	
tta agg ccg cgt ttg gat ccg ccg gct ccg ggg aac tac ttc gga aac	959
Leu Arg Pro Arg Leu Asp Pro Pro Ala Pro Gly Asn Tyr Phe Gly Asn	
305 310 315	
tgt cta tcg ttt gcg atg gcg aag atc ctg cgg cgg gat ttg gtc gga	1007
Cys Leu Ser Phe Ala Met Ala Lys Ile Leu Arg Arg Asp Leu Val Gly	
320 325 330 335	
gat gaa ggg gtg ttt ccg gca gct gag gcg atc gcg gcg gaa ata gag	1055
Asp Glu Gly Val Phe Arg Ala Ala Glu Ile Ala Ala Glu Ile Glu	
340 345 350	
aag agg acg agc gac aag aag att cta gaa act gtg gag aac tgg ccg	1103
Lys Arg Thr Ser Asp Lys Lys Ile Leu Glu Thr Val Glu Asn Trp Pro	
355 360 365	
tct gag att cgc gaa gcc ttg caa aac tgt tat ttc tcg gtg gcg gga	1151
Ser Glu Ile Arg Glu Ala Leu Gln Asn Cys Tyr Phe Ser Val Ala Gly	
370 375 380	
tcg agc agg ctt gat ctt tac ggc gcg gat ttt gga tgg ggt aag gcg	1199
Ser Ser Arg Leu Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala	
385 390 395	
gtg aag caa gag ata ctg tcg att gat gga gag aag ttt acg atg tcg	1247
Val Lys Gln Glu Ile Leu Ser Ile Asp Gly Glu Lys Phe Thr Met Ser	
400 405 410 415	
ttg tgt aaa ccg agg gat gct gcc gga gga ttg gag gtt gga ttg tct	1295
Leu Cys Lys Pro Arg Asp Ala Ala Gly Gly Leu Glu Val Gly Leu Ser	
420 425 430	
ttg cca aag gag gaa ttg caa gct ttt gat gat tat ttt gcg gag gga	1343
Leu Pro Lys Glu Glu Leu Gln Ala Phe Asp Asp Tyr Phe Ala Glu Gly	
435 440 445	
ata aag ggt tgattaatca tttaatcatg tattatgaag ttggatgaaa	1392
Ile Lys Gly	
450	
tcctctgttt catctctatt gtttaaacaa taattttttt ccattgaact tttttgagtc	1452
aataaaaaaaaa aaaaaaaaaa aaaaaaatg aaaaaactca gttattttttt tttttttttt	1512
tttttttttt	1521

<210> 7
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 7
 Arg Phe Leu Gly Ile Thr Gly Ser Pro Lys
 1 5 10

<210> 8
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 8
 Ile His Met Asp Ala Phe Ala Lys
 1 5

<210> 9
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 9
 Gly Val Glu Ile Gly Val Ser Leu Pro Lys
 1 5 10

<210> 10
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 10
 Ala Ser Leu Ser Leu Thr Leu Lys
 1 5

<210> 11
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 11
 His Tyr Val Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys
 1 5 10

<210> 12
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 12
 Val Arg Ala Thr Tyr Val Leu Ser Leu Ala Glu Ile Gln Lys
 1 5 10

<210> 13
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 13
 Ile His Met Asp Ala Phe Ala Lys
 1 5

<210> 14
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 14
 Lys Ile His Met Asp Ala Phe Ala Lys
 1 5

<210> 15
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 15
 Lys Ile His Met Asp Ala Phe Ala
 1 5

<210> 16
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
 <221> modified_base
 <222> (18)
 <223> a, c, g, t, unknown, or other

<400> 16
 aarathcaya tggaygcntt ygc

23

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 17
 ctcgagt ttt tttttttttt ttt

23

<210> 18
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18
 ttcacatgg agcaaattcca aatggt

26

<210> 19
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 19
 cgagtcgccc tcatcac

17

<210> 20
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 20
 aacagctatg accatg

16

<210> 21
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 21
 Asp Phe Gly Trp Gly Lys
 1 5

<210> 22
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> modified_base
 <222> (9)
 <223> a, c, g, t, unknown, or other

<220>
 <221> modified_base
 <222> (15)
 <223> a, c, g, t, unknown, or other

<400> 22
 gayttyggnt ggggnaa 17

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 23
 tggcaactgt cttgcgtcat g 21

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 24
 ccatgtcagg tgtgagggttc aac 23

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 25
 atcgtttcgc atgattgaac 20

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 26
 tcagaagaac tcgtcaagaa 20

<210> 27
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide

<220>
 <221> CDS
 <222> (12)..(53)

<400> 27
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 Met Glu Gln Ile Gln Met Val Ala Val Ile Glu Thr Cys
 1 5 10

aga 53
 Arg

<210> 28
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 28
 gtaaaacgac ggccat 16

<210> 29
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide

<220>
 <221> CDS
 <222> (12)..(44)

<400> 29
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 Met Glu Gln Ile Gln Met Val Asn Ile Leu Glu
 1 5 10

<210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 30
 ctcggaggaa ttcggcacga c

21

<210> 31
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide

<220>
 <221> CDS
 <222> (18)..(35)

<400> 31
 agtcggatcc aacaatg acc acc ctc ctc gaa tcc
 Thr Thr Leu Leu Glu Ser
 1 5

35

<210> 32
 <211> 469
 <212> PRT
 <213> Gentiana triflora

<400> 32
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 1 5 10 15
 Pro Pro Ser Asp Thr Thr Asp Val Glu Leu Ser Leu Pro Val Thr Phe
 20 25 30
 Phe Asp Ile Pro Trp Leu His Leu Asn Lys Met Gln Ser Leu Leu Phe
 35 40 45
 Tyr Asp Phe Pro Tyr Pro Arg Thr His Phe Leu Asp Thr Val Ile Pro
 50 55 60
 Asn Leu Lys Ala Ser Leu Ser Leu Thr Leu Lys His Tyr Val Pro Leu
 65 70 75 80
 Ser Gly Asn Leu Leu Met Pro Ile Lys Ser Gly Glu Met Pro Lys Phe
 85 90 95

Gln	Tyr	Ser	Arg	Asp	Glu	Gly	Asp	Ser	Ile	Thr	Leu	Ile	Val	Ala	Glu	100	105	110	
Ser	Asp	Gln	Asp	Phe	Asp	Tyr	Leu	Lys	Gly	His	Gln	Leu	Val	Asp	Ser	115	120	125	
Asn	Asp	Leu	His	Gly	Leu	Phe	Tyr	Val	Met	Pro	Arg	Val	Ile	Arg	Thr	130	135	140	
Met	Gln	Asp	Tyr	Lys	Val	Ile	Pro	Leu	Val	Ala	Val	Gln	Val	Thr	Val	145	150	155	160
Phe	Pro	Asn	Arg	Gly	Ile	Ala	Val	Ala	Leu	Thr	Ala	His	His	Ser	Ile	165	170	175	
Ala	Asp	Ala	Lys	Ser	Phe	Val	Met	Phe	Ile	Asn	Ala	Trp	Ala	Tyr	Ile	180	185	190	
Asn	Lys	Phe	Gly	Lys	Asp	Ala	Asp	Leu	Leu	Ser	Ala	Asn	Leu	Leu	Pro	195	200	205	
Ser	Phe	Asp	Arg	Ser	Ile	Ile	Lys	Asp	Leu	Tyr	Gly	Leu	Glu	Glu	Thr	210	215	220	
Phe	Trp	Asn	Glu	Met	Gln	Asp	Val	Leu	Glu	Met	Phe	Ser	Arg	Phe	Gly	225	230	235	240
Ser	Lys	Pro	Pro	Arg	Phe	Asn	Lys	Val	Arg	Ala	Thr	Tyr	Val	Leu	Ser	245	250	255	
Leu	Ala	Glu	Ile	Gln	Lys	Leu	Lys	Asn	Lys	Val	Leu	Asn	Leu	Arg	Gly	260	265	270	
Ser	Glu	Pro	Thr	Ile	Arg	Val	Thr	Thr	Phe	Thr	Met	Thr	Cys	Gly	Tyr	275	280	285	
Val	Trp	Thr	Cys	Met	Val	Lys	Ser	Lys	Asp	Asp	Val	Val	Ser	Glu	Glu	290	295	300	
Ser	Ser	Asn	Asp	Glu	Asn	Glu	Leu	Glu	Tyr	Phe	Ser	Phe	Thr	Ala	Asp	305	310	315	320
Cys	Arg	Gly	Leu	Leu	Thr	Pro	Pro	Cys	Pro	Pro	Asn	Tyr	Phe	Gly	Asn	325	330	335	
Cys	Leu	Ala	Ser	Cys	Val	Ala	Lys	Ala	Thr	His	Lys	Glu	Leu	Val	Gly	340	345	350	
Asp	Lys	Gly	Leu	Leu	Val	Ala	Val	Ala	Ala	Ile	Gly	Glu	Ala	Ile	Glu	355	360	365	
Lys	Arg	Leu	His	Asn	Glu	Lys	Gly	Val	Leu	Ala	Asp	Ala	Lys	Thr	Trp	370	375	380	
Leu	Ser	Glu	Ser	Asn	Gly	Ile	Pro	Ser	Lys	Arg	Phe	Leu	Gly	Ile	Thr	385	390	395	400

Gly Ser Pro Lys Phe Asp Ser Tyr Gly Val Asp Phe Gly Trp Gly Lys
 405 410 415
 Pro Ala Lys Phe Asp Ile Thr Ser Val Asp Tyr Ala Glu Leu Ile Tyr
 420 425 430
 Val Ile Gln Ser Arg Asp Phe Glu Lys Gly Val Glu Ile Gly Val Ser
 435 440 445
 Leu Pro Lys Ile His Met Asp Ala Phe Ala Lys Ile Phe Glu Glu Gly
 450 455 460
 Phe Cys Ser Leu Ser
 465

<210> 33
 <211> 479
 <212> PRT
 <213> Gentiana triflora

<400> 33
 Met Ala Gly Asn Ser Glu Asp Ile Lys Val Leu Glu Lys Cys Arg Val
 1 5 10 15
 Ala Pro Pro Pro Asp Ala Val Ala Glu Phe Thr Val Pro Leu Ser Phe
 20 25 30
 Phe Asp Met Arg Trp Leu Ile Ser Asp Ala Glu His His Leu His Phe
 35 40 45
 Tyr Arg Phe Arg His Pro Cys Pro Asn Ser Lys Phe Ile Ile Ser Ser
 50 55 60
 Ile Lys Ser Ser Leu Ser Leu Val Leu Lys His Phe Leu Pro Leu Ala
 65 70 75 80
 Gly Asn Leu Ile Trp Pro Val Asp Ser Ser Asp Arg Met Pro Glu Leu
 85 90 95
 Arg Tyr Lys Lys Gly Asp Ser Val Ser Leu Thr Ile Ala Glu Ser Ser
 100 105 110
 Met Asp Phe Asp Tyr Leu Ala Gly Asp His Gln Arg Asp Ser Tyr Lys
 115 120 125
 Phe Asn Asp Leu Ile Pro Gln Leu Pro Glu Pro Ile Val Thr Ser Gly
 130 135 140
 Asp Glu Val Leu Pro Leu Phe Ala Leu Gln Val Thr Val Phe Ser Asn
 145 150 155 160
 Thr Gly Ile Cys Ile Gly Arg Asn Leu His Gln Val Leu Gly Asp Ala
 165 170 175
 Ser Ser Phe Leu His Phe Asn Lys Leu Trp Val Leu Val Asp Lys Ser
 180 185 190

Asn Gly Asp Ser Leu Lys Phe Leu Pro Leu Ser Ser Leu Pro Met Tyr
 195 200 205
 Asp Arg Ser Val Val Gln Asp Pro Phe His Ile Arg Arg Lys Ile Tyr
 210 215 220
 Asn Glu Arg Lys Leu Leu Lys Ser Gln Gly Thr Pro Thr Val Leu Asn
 225 230 235 240
 Pro Ala Ile Ser Lys Asp Glu Val Arg Ala Thr Phe Ile Leu His Pro
 245 250 255
 Ile Asp Ile Met Lys Leu Lys Lys Phe Ile Ser Ser Lys Asn Arg Asn
 260 265 270
 Leu Thr Gly Ser Ser Asn Tyr Asn Leu Ser Thr Phe Thr Val Thr Ser
 275 280 285
 Ala Leu Ile Trp Thr Cys Leu Ser Lys Ser Leu Asp Thr Val Val Arg
 290 295 300
 Glu Lys Val Glu Glu Asp Lys His Ala Ala Asn Leu Cys Ala Phe Ile
 305 310 315 320
 Asn Cys Arg Gln Arg Phe Ala Pro Pro Ile Pro Gln Asn Tyr Phe Gly
 325 330 335
 Asn Cys Ile Val Pro Cys Met Val Gly Ser Thr His Glu Gln Leu Val
 340 345 350
 Gly Asn Glu Gly Leu Ser Val Ala Ala Thr Ala Ile Gly Asp Ala Ile
 355 360 365
 His Lys Arg Leu His Asp Tyr Glu Gly Ile Leu Arg Gly Asp Trp Ile
 370 375 380
 Ser Pro Pro Arg Ser Thr Ser Ala Ala Pro Arg Ser Thr Leu Ile Tyr
 385 390 395 400
 Val Val Gly Ser Ala Gln Arg Asn Val His Asp Phe Asp Ala Asp Phe
 405 410 415
 Gly Trp Gly Lys Leu Glu Lys His Glu Ser Val Ser Thr Asn Pro Ser
 420 425 430
 Ala Thr Leu Ile Leu Ile Ser Arg Ser Arg Arg Phe Lys Gly Ala Leu
 435 440 445
 Glu Leu Gly Ile Ser Leu Pro Lys Asn Arg Met Asp Ala Phe Ala Thr
 450 455 460
 Ile Phe Thr Asn Phe Ile Asn Ser Leu His Val Arg Ser Pro Leu
 465 470 475

<210> 34
 <211> 448
 <212> PRT
 <213> Petunia hybrida

<400> 34

Met	Ala	Gly	Glu	Val	Ala	Lys	Gln	Glu	Val	Thr	Lys	Val	Lys	Val	Leu
1				5					10					15	
Lys	Lys	Thr	Asn	Val	Lys	Pro	His	Lys	Pro	Leu	Gly	Lys	Lys	Glu	Cys
			20					25					30		
Gln	Leu	Val	Thr	Phe	Asp	Leu	Pro	Tyr	Leu	Ala	Phe	Tyr	Tyr	Asn	Gln
		35					40					45			
Lys	Phe	Leu	Ile	Tyr	Lys	Gly	Ala	Glu	Asn	Phe	Asp	Glu	Thr	Val	Glu
	50					55					60				
Lys	Ile	Lys	Asp	Gly	Leu	Ala	Leu	Val	Leu	Val	Asp	Phe	Tyr	Gln	Leu
65					70					75					80
Ala	Gly	Lys	Leu	Gly	Lys	Asp	Glu	Glu	Gly	Val	Phe	Arg	Val	Glu	Tyr
				85					90					95	
Asp	Asp	Asp	Met	Asp	Gly	Val	Glu	Val	Thr	Val	Ala	Val	Ala	Glu	Glu
			100					105					110		
Ile	Glu	Val	Ala	Asp	Leu	Thr	Asp	Glu	Glu	Gly	Thr	Thr	Lys	Leu	Gln
		115					120					125			
Asp	Leu	Ile	Pro	Cys	Asn	Lys	Ile	Leu	Asn	Leu	Glu	Gly	Leu	His	Arg
	130					135					140				
Pro	Leu	Leu	Ala	Val	Gln	Leu	Thr	Lys	Leu	Lys	Asp	Gly	Leu	Thr	Met
145					150					155					160
Gly	Leu	Ala	Phe	Asn	His	Ala	Val	Leu	Asp	Gly	Thr	Ser	Thr	Trp	His
				165					170					175	
Phe	Met	Thr	Ser	Trp	Ser	Glu	Leu	Cys	Cys	Gly	Ser	Thr	Ser	Ile	Ser
			180					185					190		
Val	Pro	Pro	Phe	Leu	Glu	Arg	Thr	Lys	Ala	Arg	Asn	Thr	Arg	Val	Lys
		195					200					205			
Leu	Asn	Leu	Ser	Gln	Pro	Ser	Asp	Ala	Pro	Glu	His	Ala	Lys	Ser	Ala
	210					215					220				
Thr	Asn	Gly	Asp	Val	Pro	Ala	Asn	Val	Asp	Pro	Pro	Leu	Arg	Glu	Arg
225					230					235				240	
Val	Phe	Lys	Phe	Ser	Glu	Leu	Ala	Ile	Asp	Lys	Ile	Lys	Ser	Thr	Val
				245					250					255	
Asn	Ala	Asn	Ser	Gly	Glu	Thr	Pro	Phe	Ser	Thr	Phe	Gln	Ser	Leu	Ser
			260					265					270		

Ala His Val Trp Leu Ala Val Thr Arg Ala Arg Gln Leu Lys Pro Glu
 275 280 285

Asp Tyr Thr Val Tyr Thr Val Phe Ala Asp Cys Arg Lys Arg Val Asp
 290 295 300

Pro Pro Met Pro Glu Ser Tyr Phe Gly Asn Leu Ile Gln Ala Ile Phe
 305 310 315 320

Thr Val Thr Ala Ala Gly Leu Leu Leu Ala Ser Pro Ile Glu Phe Ala
 325 330 335

Gly Gly Met Ile Gln Gln Ala Ile Val Lys His Asp Ala Lys Ala Ile
 340 345 350

Asp Glu Arg Asn Lys Glu Trp Glu Ser Asn Pro Lys Ile Phe Gln Tyr
 355 360 365

Lys Asp Ala Gly Val Asn Cys Val Ala Val Gly Ser Ser Pro Arg Phe
 370 375 380

Lys Val Tyr Asp Val Asp Phe Gly Trp Gly Lys Pro Glu Ser Val Arg
 385 390 395 400

Ser Gly Ser Asn Asn Arg Phe Asp Gly Met Val Tyr Leu Tyr Gln Gly
 405 410 415

Lys Asn Gly Gly Arg Ser Ile Asp Val Glu Ile Ser Leu Glu Ala Asn
 420 425 430

Ala Met Glu Arg Leu Glu Lys Asp Lys Glu Phe Leu Met Glu Thr Ala
 435 440 445

<210> 35
 <211> 446
 <212> PRT
 <213> Perilla ocimoides

<400> 35
 Val Ile Glu Thr Cys Arg Val Gly Pro Pro Pro Asp Ser Val Ala Glu
 1 5 10 15

Gln Ser Val Pro Leu Thr Phe Phe Asp Met Thr Trp Leu His Phe His
 20 25 30

Pro Met Leu Gln Leu Leu Phe Tyr Glu Phe Pro Cys Ser Lys Gln His
 35 40 45

Phe Ser Glu Ser Ile Val Pro Lys Leu Lys Gln Ser Leu Ser Lys Thr
 50 55 60

Leu Ile His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr Pro Ser Ser
 65 70 75 80

Pro Glu Lys Met Pro Glu Phe Arg Tyr Leu Ser Gly Asp Ser Val Ser
 85 90 95

Phe	Thr	Ile	Ala	Glu	Ser	Ser	Asp	Asp	Phe	Asp	Asp	Leu	Val	Gly	Asn		
			100					105					110				
Arg	Pro	Glu	Ser	Pro	Val	Arg	Leu	Tyr	Asn	Phe	Val	Pro	Lys	Leu	Pro		
		115					120					125					
Pro	Ile	Val	Glu	Glu	Ser	Asp	Arg	Lys	Leu	Phe	Gln	Val	Phe	Ala	Val		
	130					135					140						
Gln	Val	Thr	Leu	Phe	Pro	Gly	Arg	Gly	Val	Gly	Ile	Gly	Ile	Ala	Thr		
145					150					155					160		
His	His	Thr	Val	Ser	Asp	Ala	Pro	Ser	Phe	Leu	Ala	Phe	Ile	Thr	Ala		
			165						170					175			
Trp	Ser	Ser	Met	Ser	Lys	His	Ile	Glu	Asn	Glu	Asp	Glu	Asp	Glu	Glu		
			180					185					190				
Phe	Lys	Ser	Leu	Pro	Val	Phe	Asp	Arg	Ser	Val	Ile	Lys	Tyr	Pro	Thr		
		195					200					205					
Lys	Phe	Asp	Ser	Ile	Tyr	Trp	Arg	Asn	Ala	Leu	Lys	Phe	Pro	Leu	Gln		
	210					215					220						
Ser	Arg	His	Pro	Ser	Leu	Pro	Thr	Asp	Arg	Ile	Arg	Thr	Thr	Phe	Val		
225					230					235					240		
Phe	Thr	Gln	Ser	Lys	Ile	Lys	Lys	Leu	Lys	Gly	Trp	Ile	Gln	Ser	Arg		
				245					250					255			
Val	Pro	Ser	Leu	Val	His	Leu	Ser	Ser	Phe	Val	Ala	Ile	Ala	Ala	Tyr		
			260					265					270				
Met	Trp	Ala	Gly	Ile	Thr	Lys	Ser	Phe	Thr	Ala	Asp	Glu	Asp	Gln	Asp		
		275					280					285					
Asn	Glu	Asp	Ala	Phe	Phe	Leu	Ile	Pro	Val	Asp	Leu	Arg	Pro	Arg	Leu		
	290					295					300						
Asp	Pro	Pro	Val	Pro	Glu	Asn	Tyr	Phe	Gly	Asn	Cys	Leu	Ser	Tyr	Ala		
305					310					315					320		
Leu	Pro	Arg	Met	Arg	Arg	Arg	Glu	Leu	Val	Gly	Glu	Lys	Gly	Val	Phe		
				325					330					335			
Leu	Ala	Ala	Glu	Val	Ile	Ala	Ala	Glu	Ile	Lys	Lys	Arg	Ile	Asn	Asp		
			340					345					350				
Lys	Arg	Ile	Leu	Glu	Thr	Val	Glu	Lys	Trp	Ser	Pro	Glu	Ile	Arg	Lys		
		355					360					365					
Ala	Leu	Gln	Lys	Ser	Tyr	Phe	Ser	Val	Ala	Gly	Ser	Ser	Lys	Leu	Asp		
	370					375					380						
Leu	Tyr	Gly	Ala	Asp	Phe	Gly	Trp	Gly	Lys	Ala	Arg	Lys	Gln	Glu	Ile		
385					390					395					400		

Leu Ser Ile Asp Gly Glu Lys Tyr Ala Met Thr Leu Cys Lys Ala Arg
 405 410 415

Asp Phe Glu Gly Gly Leu Glu Val Cys Leu Ser Leu Pro Lys Asp Lys
 420 425 430

Met Asp Ala Phe Ala Ala Tyr Phe Ser Leu Gly Ile Asn Gly
 435 440 445

<210> 36

<211> 454

<212> PRT

<213> Senecio cruentus

<400> 36

Asn Ile Leu Glu His Ala Arg Ile Ser Ala Pro Ser Gly Thr Ile Gly
 1 5 10 15

His Arg Ser Leu Ser Leu Thr Phe Phe Asp Ile Thr Trp Leu Leu Phe
 20 25 30

Pro Pro Val His His Leu Phe Phe Tyr Asp Phe Pro His Ser Lys Ser
 35 40 45

His Phe Met Asp Thr Ile Val Pro Arg Leu Lys Gln Ser Leu Ser Val
 50 55 60

Thr Leu Gln His Phe Phe Pro Phe Ala Ser Asn Leu Ile Val Phe Pro
 65 70 75 80

Asn Thr Asp Gly Ser Gly Phe Asn Lys Lys Pro Glu Ile Lys His Val
 85 90 95

Glu Gly Asp Ser Val Val Val Thr Phe Ala Glu Cys Cys Leu Asp Phe
 100 105 110

Asn Asn Leu Thr Gly Asn His Pro Arg Lys Cys Glu Asn Phe Tyr Pro
 115 120 125

Leu Val Pro Ser Leu Gly Asn Ala Ile Lys Leu Cys Asp Cys Val Thr
 130 135 140

Val Pro Leu Phe Ser Leu Gln Val Thr Phe Phe Pro Gly Ser Gly Ile
 145 150 155 160

Ser Leu Gly Met Thr Asn His His Ser Leu Gly Asp Ala Ser Thr Arg
 165 170 175

Phe Asn Phe Leu Lys Gly Trp Thr Ser Ile Ile Gln Ser Gly Val Asp
 180 185 190

Arg Ser Phe Leu Thr Lys Gly Ser Pro Pro Val Phe Asp Arg Leu Ile
 195 200 205

Asn Ile Pro His Leu Asp Glu Asn Lys Leu Arg His Thr Arg Leu Glu
 210 215 220

Ser Phe Tyr Lys Pro Ser Ser Leu Val Gly Pro Thr Asp Lys Val Arg
 225 230 235 240
 Ser Thr Phe Val Leu Thr Arg Thr Asn Ile Asn Leu Leu Lys Lys Lys
 245 250 255
 Val Leu Thr Gln Val Pro Asn Leu Glu Tyr Met Ser Ser Phe Thr Val
 260 265 270
 Thr Cys Gly Tyr Ile Trp Ser Cys Ile Ala Lys Ser Leu Val Lys Ile
 275 280 285
 Gly Glu Arg Lys Gly Glu Asp Glu Leu Glu Gln Phe Ile Ile Thr Ile
 290 295 300
 Asp Cys Arg Ser Arg Leu Asp Pro Pro Ile Pro Thr Ala Tyr Phe Gly
 305 310 315 320
 Asn Cys Gly Ala Pro Cys Val Pro Thr Leu Lys Asn Val Val Leu Thr
 325 330 335
 Thr Glu Asn Gly Tyr Ala Leu Gly Ala Lys Val Ile Gly Glu Ser Ile
 340 345 350
 Cys Lys Met Ile Tyr Asn Lys Asp Gly Ile Leu Lys Asp Ala Ala Arg
 355 360 365
 Trp His Glu Pro Phe Met Ile Pro Ala Arg Lys Ile Gly Val Ala Gly
 370 375 380
 Thr Pro Lys Leu Asn Leu Tyr Asp Phe Asp Phe Gly Trp Gly Lys Arg
 385 390 395 400
 Ile Lys Tyr Glu Thr Val Ser Ile Asp Tyr Asn Thr Ser Ile Ser Ile
 405 410 415
 Asn Ala Ser Lys Thr Ser Ala Gln Asp Leu Glu Ile Gly Leu Ser Leu
 420 425 430
 Pro Ser Met Gln Met Glu Ala Phe Ser Ser Ile Phe Asp Glu Gly Leu
 435 440 445
 Glu Ser Gln Val Ser Leu
 450

<210> 37

<211> 450

<212> PRT

<213> *Lavandula angustifolia*

<400> 37

Thr Thr Leu Leu Glu Ser Ser Arg Val Ala Pro Pro Pro Gly Thr Val
 1 5 10 15
 Ala Glu Gln Ser Leu Pro Leu Thr Phe Phe Asp Met Thr Trp Leu His
 20 25 30

Phe His Pro Met Leu Gln Leu Leu Phe Tyr Glu Leu Pro Cys Ser Lys
 35 40 45

Pro Ala Phe Leu Glu Thr Val Val Pro Lys Leu Lys Gln Ser Leu Ser
 50 55 60

Leu Thr Leu Lys His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr Pro
 65 70 75 80

Leu Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Gln Asn Gly Asp Ser
 85 90 95

Val Ser Phe Thr Ile Met Glu Ser Val Gly Asp His Pro His Ser Ala
 100 105 110

His Lys Tyr Tyr Cys Phe Ala Pro Ser Asp Asp Tyr Glu Asp Leu Gln
 115 120 125

Leu Pro Pro Ile Val Glu Glu Ser Asp Arg Lys Leu Phe Gln Val Leu
 130 135 140

Ala Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Cys Ile Gly Ile
 145 150 155 160

Thr Thr His His Thr Val Ser Asp Ala Pro Ser Phe Val Gly Phe Met
 165 170 175

Lys Ser Trp Ala Ser Ile Thr Lys Phe Gly Gly Asp Asp Glu Phe Leu
 180 185 190

Asp Gly Lys Gly Glu Cys Leu Pro Val Phe Asp Arg Ser Leu Val Asn
 195 200 205

Tyr Pro Pro Lys Leu Asp Thr Tyr Leu Trp Asn Asn Ala Gln Lys Arg
 210 215 220

Pro Leu Glu Ser Gln His Pro Ser Leu Pro Thr Asp Arg Ile Arg Ala
 225 230 235 240

Thr Tyr Leu Phe Thr Gln Ser Glu Ile Lys Lys Leu Lys Gly Leu Ile
 245 250 255

Gln Arg Lys Ala Pro Asn Val Val Asn Leu Ser Ser Phe Val Ala Ile
 260 265 270

Ala Ala Tyr Ile Trp Thr Gly Ile Ala Lys Ser Val Gly Asp Tyr Lys
 275 280 285

Asp Val Asp Asp Asp Lys Arg Ala Phe Phe Leu Ile Pro Ile Asp Leu
 290 295 300

Arg Pro Arg Leu Asp Pro Pro Ala Pro Gly Asn Tyr Phe Gly Asn Cys
 305 310 315 320

Leu Ser Phe Ala Met Ala Lys Ile Leu Arg Arg Asp Leu Val Gly Asp
 325 330 335

Glu Gly Val Phe Arg Ala Ala Glu Ala Ile Ala Ala Glu Ile Glu Lys
 340 345 350

Arg Thr Ser Asp Lys Lys Ile Leu Glu Thr Val Glu Asn Trp Pro Ser
 355 360 365

Glu Ile Arg Glu Ala Leu Gln Asn Cys Tyr Phe Ser Val Ala Gly Ser
 370 375 380

Ser Arg Leu Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala Val
 385 390 395 400

Lys Gln Glu Ile Leu Ser Ile Asp Gly Glu Lys Phe Thr Met Ser Leu
 405 410 415

Cys Lys Pro Arg Asp Ala Ala Gly Gly Leu Glu Val Gly Leu Ser Leu
 420 425 430

Pro Lys Glu Glu Leu Gln Ala Phe Asp Asp Tyr Phe Ala Glu Gly Ile
 435 440 445

Lys Gly
 450

<210> 38

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 38

Met Glu Gln Ile Gln Met Val Ala Val Ile Glu Thr Cys Arg
 1 5 10

<210> 39

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 39

Met Glu Gln Ile Gln Met Val Asn Ile Leu Glu
 1 5 10

<210> 40

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 40

Thr Thr Leu Leu Glu Ser
1 5